

VW

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PCT09

RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/856,050

TIME: 09:50:56

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\10112001\I856050.raw

ENTERED

3 <110> APPLICANT: UEMURA, Hidetoshi
 4 OKUI, Akira
 5 KOMINAMI, Katsuya
 6 YAMAGUCHI, Nozomi
 7 MITSUI, Shinichi
 9 <120> TITLE OF INVENTION: PROTEIN EXPRESSION VECTOR AND USE THEREOF
 11 <130> FILE REFERENCE: UEMURA=8
 13 <140> CURRENT APPLICATION NUMBER: 09/856,050
 14 <141> CURRENT FILING DATE: 2001-05-17
 16 <150> PRIOR APPLICATION NUMBER: JP 10/331515
 17 <151> PRIOR FILING DATE: 1998-11-20
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/06474
 20 <151> PRIOR FILING DATE: 1999-11-19
 22 <160> NUMBER OF SEQ ID NOS: 22
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
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 28 <212> TYPE: DNA
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 35 <221> NAME/KEY: misc_feature
 36 <223> OTHER INFORMATION: Designed oligonucleotide to construct plasmid pTrypHis
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 47 <212> TYPE: DNA
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 69 <220> FEATURE:
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 72 <220> FEATURE:
 73 <221> NAME/KEY: misc_feature

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74 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify neurosin-encoding
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75     ence
78 <400> SEQUENCE: 3
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91 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify neurosin-encoding
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92     ence
93 <400> SEQUENCE: 4
94 ggaattcact tggcctgaat                                20
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98 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
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101 <220> FEATURE:
102 <221> NAME/KEY: misc_feature
103 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
plasmid p
104     TrypHis/Neurosin
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106 ctaagcttga cgacgatgac aagttg                                26
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109 <212> TYPE: DNA
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116 <211> LENGTH: 26
117 <212> TYPE: DNA
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120 <223> OTHER INFORMATION: Synthetic OK
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123 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
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125 <400> SEQUENCE: 7
126 ccaagcttca ccatcaccat caccat                                26
127 <210> SEQ ID NO: 8

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156 <220> FEATURE:
157 <221> NAME/KEY: misc_feature
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164 tgctgcccc tttgacgacg atgacaagga tccgaattc      99
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175 <220> FEATURE:
176 <221> NAME/KEY: misc_feature
177 <223> OTHER INFORMATION: Designed oligonucleotide to construct plasmid pSecTrypHis
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192 <223> OTHER INFORMATION: Synthetic OK
194 <220> FEATURE:
195 <221> NAME/KEY: misc_feature
196 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
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205 <211> LENGTH: 29
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
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212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify a portion of
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222 <210> SEQ ID NO: 12
223 <211> LENGTH: 17

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228 <223> OTHER INFORMATION: Synthetic OK
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243 <213> ORGANISM: Artificial Sequence
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261 <213> ORGANISM: Homo sapiens
263 <220> FEATURE:
264 <221> NAME/KEY: CDS
265 <222> LOCATION: (1)..(672)
266 <223> OTHER INFORMATION:
269 <400> SEQUENCE: 14
270 ttg gtg cat ggc gga ccc tgc gac aag aca tct cac ccc tac caa gct 48
271 Leu Val His Gly Gly Pro Cys Asp Lys Thr Ser His Pro Tyr Gln Ala
272 1 5 10 15
274 gcc ctc tac acc tcg ggc cac ttg ctc tgt ggt ggg gtc ctt atc cat 96
275 Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly Gly Val Leu Ile His
276 20 25 30
278 cca ctg tgg gtc ctc aca gct gcc cac tgc aaa aaa ccg aat ctt cag 144
279 Pro Leu Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln
280 35 40 45
282 gtc ttc ctg ggg aag cat aac ctt cgg caa agg gag agt tcc cag gag 192
283 Val Phe Leu Gly Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
284 50 55 60
286 cag agt tct gtt gtc cgg gct gtg atc cac cct gac tat gat gcc gcc 240
287 Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala Ala
288 65 70 75 80
290 agc cat gac cag gac atc atg ctg ttg cgc ctg gca cgc cca gcc aaa 288
291 Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro Ala Lys
292 85 90 95

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294 ctc tct gaa ctc atc cag ccc ctt ccc ctg gag agg gac tgc tca gcc      336
295 Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp Cys Ser Ala
296          100          105          110
298 aac acc acc agc tgc cac atc ctg ggc tgg ggc aag aca gca gat ggt      384
299 Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly Lys Thr Ala Asp Gly
300          115          120          125
302 gat ttc cct gac acc atc cag tgt gca tac atc cac ctg gtg tcc cgt      432
303 Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile His Leu Val Ser Arg
304          130          135          140
306 gag gag tgt gag cat gcc tac cct ggc cag atc acc cag aac atg ttg      480
307 Glu Glu Cys Glu His Ala Tyr Pro Gly Gln Ile Thr Gln Asn Met Leu
308 145          150          155          160
310 tgt gct ggg gat gag aag tac ggg aag gat tcc tgc cag ggt gat tct      528
311 Cys Ala Gly Asp Glu Lys Tyr Gly Lys Asp Ser Cys Gln Gly Asp Ser
312          165          170          175
314 ggg ggt ccg ctg gta tgt gga gac cac ctc cga ggc ctt gtg tca tgg      576
315 Gly Gly Pro Leu Val Cys Gly Asp His Leu Arg Gly Leu Val Ser Trp
316          180          185          190
318 ggt aac atc ccc tgt gga tca aag gag aag cca gga gtc tac acc aac      624
319 Gly Asn Ile Pro Cys Gly Ser Lys Glu Lys Pro Gly Val Tyr Thr Asn
320          195          200          205
322 gtc tgc aga tac acg aac tgg atc caa aaa acc att cag gcc aag tga      672
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324          210          215          220
327 <210> SEQ ID NO: 15
328 <211> LENGTH: 223
329 <212> TYPE: PRT
330 <213> ORGANISM: Homo sapiens
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Synthetic 04
335 <400> SEQUENCE: 15
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338 1          5          10          15
341 Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly Gly Val Leu Ile His
342          20          25          30
345 Pro Leu Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln
346          35          40          45
349 Val Phe Leu Gly Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
350          50          55          60
353 Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala Ala
354 65          70          75          80
357 Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro Ala Lys
358          85          90          95
361 Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp Cys Ser Ala
362          100          105          110
365 Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly Lys Thr Ala Asp Gly
366          115          120          125
369 Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile His Leu Val Ser Arg
370          130          135          140

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VERIFICATION SUMMARY

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